

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
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(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS  
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

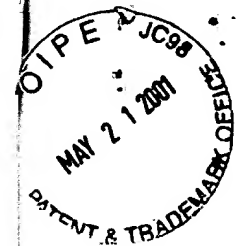
(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAAC TTTCCA TGAAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCTCCGC CAATCAGTCG	180
TAAAACAGAA GTCGTGGAAG GCGGATAGAA AGAATGTTTCG ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTCCTGTC CAGATCGAAC TCAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTCATGTTA GTTTCGCGCT	420
GAGCAACAAT TAAGTTTATG TTTCAGTTCG GCTTAGATTT CGCTGAAGGA CTGCCACTT	480
TCAATCAATA CTTTAGAACA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTTT	540
TTTTAATGAT AAGCATTTTG TCGTTTATAC TTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCATTT TAATCGCCAG ATAAGCAATA TATTGTGTAA ATATTTGTAT TCTTTATCAG	660
GAAATTCAGG GAGACGGGGA AGTTACTATC TACTAAAAGC CAAACAATTT CTTACAGTTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCG ATGTGACTAG CTCTTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCGCATGC CCCATGTGCC CCACCAAGAG	180
TTTTGCATCC CATAACAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC	240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT	300
GAATCGAAGC AAAGACCCGT GTGTAAAGCC GCGTTTCCAA AATGTATAAA ACCGAGAGCA	360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA	420
CTAAAGG	427

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA	35
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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGATCCT CATAAAGGCC CTGGGTGTC	29
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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGTTGCAGG	ACAGGATGTG	GTGCCCCGATG	TGACTAGCTC	TTTGCTGCAG	GCCGTCCTAT	60
CCTCTGGTTC	CGATAAGAGA	CCCAGAACTC	CGGCCCCCCA	CGGCCCACCG	CCACCCCAT	120
ACATATGTGG	TACGCAAGTA	AGAGTGCCTG	CGCATGCCCC	ATGTGCCCCA	CCAAGAGTTT	180
TGCATCCCAT	ACAAGTCCCC	AAAGTGGAGA	ACCGAACCAA	TTCTTCGCGG	GCAGAACAAA	240
AGCTTCTGCA	CACGTCTCCA	CTCGAATTTG	GAGCCGGCCG	GCGTGTGCAA	AAGAGGTGAA	300
TCGAACGAAA	GACCCGTGTG	TAAAGCCGCG	TTTCCAAAAT	GTATAAAACC	GAGAGCATCT	360
GGCCAATGTG	CATCAGTTGT	GGTCAGCAGC	AAAATCAAGT	GAATCATCTC	ACTGCAACTA	420
AAGGGGGGAA	TTCTGCAGA	GACCTCCCAG	AGACCAGGAT	GCCGTGCAGC	AGAGCTCTGA	480
TTCTGGGGGT	CCTCGCCCTG	AACACCATGC	TCAGCCTCTG	CGGAGGTGAA	GACGACATTG	540
AGGCCGACCA	CGTAGGCTTC	TATGGTACAA	CTGTTTATCA	GTCTCCTGGA	GACATTGGCC	600
AGTACACACA	TGAATTTGAT	GGTGATGAGT	TGTTCTATGT	GGACTTGGAT	AAGAAGAAAA	660
CTGTCTGGAG	GCTTCCTGAG	TTTGGCCAAT	TGATACTCTT	TGAGCCCCAA	GGTGGACTGC	720
AAAACATAGC	TGCAGAAAAA	CACAAC TTGG	GAATCTTGAC	TAAGAGGTCA	AATTTACCCC	780
CAGCTACCAA	TGAGGCTCCT	CAAGCGACTG	TGTTCCCCAA	GTCCCCTGTG	CTGCTGGGTC	840
AGCCCAACAC	CCTTATCTGC	TTTGTGGACA	ACATCTTCCC	ACCTGTGATC	AACATCACAT	900
GGCTCAGGAA	TAGCAAGTCA	GTACACAGCG	GCGTTTATGA	GACCAGCTTC	CTCGTCAACC	960
GTGACCATTG	CTTCCACAAG	CTGTCTTATC	TCACCTTCAT	CCCTTCTGAT	GATGACATTT	1020
ATGACTGCAA	GGTGGAGCAC	TGGGGCCTGG	AGGAGCCGGT	TCTGAAACAC	TGGGAACCTG	1080
AGATTCCAGC	CCCCATGTCA	GAGCTGACAG	AAACTGTGGT	GTGTGCCCTG	GGGTTGTCTG	1140
TGGGCCTTGT	GGGCATCGTG	GTGGGCACCA	TCTTCATCAT	TCAAGGCCTG	CGATCAGGTG	1200
GCACCTCCAG	ACACCCAGGG	CCTTTATGAG	TCACACCCCTG	GAAAGGAAGG	TGTGTGTCCC	1260
TCTTCATGGA	AGAAGTGGTG	TTCTGGGTGT	CGAATTGAG	CTCGGTACCC	GGGGATCCTC	1320
TAGAGTCGAC	CTGCAGGCAT	GCAATTCGAT	GCACACTCAC	ATTCTTCTCC	TAATACGATA	1380
ATAAACTTT	CCATGAAAAA	TATGAAAAA	TATATGAAAA	TTGAGAAATC	CAAAAACTG	1440
ATAAACGCTC	TACTTAATTA	AAATAGATAA	ATGGGAGCGG	CAGGAATGGC	GGAGCATGGC	1500
CAAGTTCCTC	CGCCAATCAG	TCGTAAAACA	GAAGTCGTGG	AAAGCGGATA	GAAAGAATGT	1560
TCGATTTGAC	GGGCAAGCAT	GTCTGCTATG	TGGCGGATTG	CGGAGGAATT	GCACTGGAGA	1620
CCAGCAAGGT	TCTCATGACC	AAGAATATAG	CGGTGAGTGA	GCGGGAAGCT	CGGTTTCTGT	1680
CCAGATCGAA	CTCAAACTA	GTCCAGCCAG	TCGCTGTGCA	AACTAATTAA	GTAAATGAGT	1740

TTTTCATGTT	AGTTTCGGCG	TGAGCAACAA	TTAAGTTTAT	GTTTCAGTTC	GGCTTAGATT	1800
TCGCTGAAGG	ACTTGCCACT	TTCAATCAAT	ACTTTAGAAC	AAAATCAAAA	CTCATTCTAA	1860
TAGCTTGGTG	TTCATCTTTT	TTTTTAATGA	TAAGCATTTT	GTCGTTTATA	CTTTTTATAT	1920
TTCGATATTA	AACCACCTAT	GAAGTTCATT	TTAATCGCCA	GATAAGCAAT	ATATTGTGTA	1980
AATATTTGTA	TTCTTTATCA	GGAAATTCAG	GGAGACGGGG	AAGTTACTAT	CTACTAAAAG	2040
CGAAACAATT	TCTTACAGTT	TACTCTCTC	TACTCTAGAG	CTTGGCACTG	GCCGTCGTTT	2100
TACAACGTGG	TGACTGGGAA	AACCCTGGCG	TTACCCAACT	TAATCGCCTT	GCAGCACATC	2160
CCCCTTTCGC	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	2220
TGCGCAGCCT	GAATGGCGAA	TGGCGCCTGA	TGGGGTATTT	TCTCCTTACG	CATCTGTGCG	2280
GTATTTTACA	CCGCATATGG	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	2340
GGCAGCCCCG	ACACCCGCCA	ACACCCGGTG	ACGCGCCCTG	ACGGGCTTGT	CTGCTCCCGG	2400
CATCCGCTTA	CAGACAAGCT	GTGACCGTCT	CCGGGAGCTG	CATGTGTCAG	AGGTTTTTAC	2460
CGTCATCACC	GAAACGCGCG	AGACGAAAGG	GCCTCGTGAT	ACGCCTATTT	TTATAGGTTA	2520
ATGTCATGAT	AATAATGGTT	TCTTAGACGT	CAGGTGGCAC	TTTTCGGGGA	AATGTGCGCG	2580
GAACCCCTAT	TTGTTTATTT	TTCTAAATAC	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	2640
AACCCTGATA	AATGCTTCAA	TAATATTGAA	AAAGGAAGAG	TATGAGTATT	CAACATTTCC	2700
GTGTGCGCGT	TATTCCCTTT	TTTGCGGCAT	TTTGCCTTCC	TGTTTTTGCT	CACCCAGAAA	2760
CGCTGGTGAA	AGTAAAAGAT	GCTGAAGATC	AGTTGGGTGC	ACGAGTGGGT	TACATCGAAC	2820
TGGATCTCAA	CAGCGGTAAG	ATCCTTGAGA	GTTTTCGCCC	CGAAGAACGT	TTTCCAATGA	2880
TGAGCACTTT	TAAAGTTCTG	CTATGTGGCG	CGGTATTATC	CCGTATTGAC	GCCGGGCAAG	2940
AGCAACTCGG	TCGCCGCATA	CACTATTCTC	AGAATGACTT	GTTTGAGTAC	TCACCAGTCA	3000
CAGAAAAGCA	TCTTACGGAT	GGCATGACAG	TAAGAGAATT	ATGCAGTGCT	GCCATAACCA	3060
TGAGTGATAA	CACTGCGGCC	AACTTACTTC	TGACAACGAT	CGGAGGACCG	AAGGAGCTAA	3120
CCGCTTTTTT	GCACAACATG	GGGGATCATG	TAACTCGCCT	TGATCCTTGG	GAACCGGAGC	3180
TGAATGAAGC	CATACCAAAC	GACGAGCGTG	ACACCACGAT	GCCTGTAGCA	ATGGCAACAA	3240
CGTTGCGCAA	ACTATTAAC	GGCGAACTAC	TTACTCTAGC	TTCCCGGCAA	CAATTAATAG	3300
ACTGGATGGA	GGCGGATAAA	GTTGCAGGAC	CACTTCTGCG	CTCGGCCCTT	CCGGCTGGCT	3360
GTTTATTGCT	TGATAAATCT	GGAGCCGGTG	AGCGTGGGTC	TCGCGGTATC	ATTGCAGCAC	3420
TGGGGCCAGA	TGGTAAGCCC	TCCCGTATCG	TAGTTATCTA	CACGACGGGG	AGTCAGGCAA	3480
CTATGGATGA	ACGAAATAGA	CAGATCGCTG	AGATAGGTGC	CTCACTGATT	AAGCATTGGT	3540
AACTGTCAGA	CCAAGTTTAC	TCATATATAC	TTTAGATTGA	TTTAAACTT	CATTTTTAAT	3600
TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTGT	ATAATCTCAT	GACCAAAATC	CCTTAACGTG	3660
AGTTTTTCGTT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT	TCTTGAGATC	3720
CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAACAAAAAA	ACCACCGCTA	CCAGCGGTGG	3780
TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA	GGTAACTGGC	TTCAGCAGAG	3840
CGCAGATACC	AAATACTGTC	CTTCTAGTGT	AGCCGTAGTT	AGGCCACCAC	TTCAAGAACT	3900
CTGTAGCACC	GCCTACATAC	CTCGCTCTGC	TAATCCTGTT	ACCAGTGGCT	GCTGCCAGTG	3960
GCGATAAGTC	GTGTCTTACC	GGGTGGGACT	CAAGACGATA	GTTACCGGAT	AAGGCGCAGC	4020
GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCCAGCTT	GGAGCGAACG	ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG 4140  
 CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCAGGAGG GAGCTTCCAG 4200  
 GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC 4260  
 GATTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACCGGGCCT 4320  
 TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTIATCCC 4380  
 CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC 4440  
 GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA ATACGCAAAC 4500  
 CGCCTCTCCC CGCGCGTTGG CCGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT 4560  
 GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC 4620  
 AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT 4680  
 TTCACACAGG AAACAGCTAT GACCATGATT ACG 4713

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA TAGCTC TTTGCTGCAG GCGGTCCTAT 60  
 CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCGA CCGCCCACCG CCACCCCAT 120  
 ACATATGTGG TACGCAAGTA AGAGTGCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT 180  
 TGCATCCCAT ACAAGTCCCC AAAGTGAGGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA 240  
 AGCTTCTGCA CACGTCCTCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA 300  
 TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT 360  
 GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA 420  
 AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC 480  
 TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCCAG GGA CTGAGGG CGGAAACTCC 540  
 GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC 600  
 ATACGGCTCG TGACCAGATA CATCTACAAC CGGGAGGAGT ACGTGCGCTA CGACAGCGAC 660  
 GTGGGCGAGT ACCGCGCGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC 720

CAGCCGGAGA TCCTGGAGCG AACGCGGGCC GAGGTGGACA CGGCGTGCAG ACACAACTAC	780
GAGGGGCGG AGACCAGCAC CTCCCTGCGG CGGCTTGAAC AGCCCAATAT CGCCATCTCC	840
CTGTCCAGGA CAGAGGCCCT CAACCACCAC AACACTCTGG TCTGTTCCGT GACAGATTTT	900
TACCCAGCCA AGATCAAAGT GCGCTGGTTC AGGAATGGCC AGGAGGAGAC AGTGGGGGTC	960
TCATCCACAC AGCTTATTAG GAATGGGGAC TGGACCTTCC AGGTCTGGT CATGCTGGAG	1020
ATGACCCCTC ATCAGGGAGA GGTCTACACC TGCCATGTGG AGCATCCCAG CCTGAAGAGC	1080
CCCATCACTG TGGAGTGGAG GGCACAGTCC GAGTCTGCCC GGAGCAAGAT GTTGAGCGGC	1140
ATCGGGGGCT GCGTGCTTGG GGTGATCTTC CTCGGGCTCG GCCTTTTCAT CCGTCACAGG	1200
AGTCAGAAAG GACCTCGAGG CCCTCCTCCA GCAGGGCTCC TGCAGTGA CTGAGTGT	1260
TGACTCAGTT GACTGTCTCA GACTGTAAGA CCTACATGTC TCGAATTCGA GCTCGGTACC	1320
CGGGGATCCT CTAGAGTCGA CCTGCAGGCA TGCAATTCGA TGCACACTCA CATTCTTCTC	1380
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AGAAAGAATG TTCGATTGTA CGGGCAAGCA TGTCTGCTAT GTGGCGGATT GCGGAGGAAT	1620
TGCACTGGAG ACCAGCAAGG TTCTCATGAC CAAGAATATA GCGGTGAGTG AGCGGGAAGC	1680
TGGGTTTCTG TCCAGATCGA ACTCAAACT AGTCCAGCCA GTCGCTGTCG AAACATAATTA	1740
AGTAAATGAG TTTTTCATGT TAGTTTCGCG CTGAGCAACA ATTAAGTTTA TGTTCAGTT	1800
CGGCTTAGAT TTCGCTGAAG GACTTGCCAC TTTCAATCAA TACTTTAGAA CAAAAACAA	1860
ACTCATTCTA ATAGCTTGGT GTTCATCTTT TTTTAAATG ATAAGCATTT TGTGTTTAT	1920
ACTTTTATA TTTTCATATT AAACCACCTA TGAAGTTCAT TTTAATCGCC AGATAAGCAA	1980
TATATTGTGT AAATATTTGT ATTCTTTATC AGGAAATTCA GGGAGACGGG GAAGTTACTA	2040
TCTACTAAAA GCCAAACAAT TTCTTACAGT TTTACTCTCT CTACTCTAGA GCTTGGCACT	2100
GGCCCTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT	2160
TGCAGCACAT CCCCCTTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCCGA CCGATCGCCC	2220
TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCCTG ATGCGGTATT TTCTCCTTAC	2280
GCATCTGTGC GGTATTTTAC ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC	2340
CGCATAGTTA AGCCAGCCCC GACACCGGCC AACACCGCCT GACGCGCCCT GACGGGCTTG	2400
TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA	2460
GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGACGAAAG GGCCTCGTGA TACGCCTATT	2520
TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG	2580
AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT	2640
CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT	2700
TCAACATTTT CCGTTCGCCC TTATTCCTTT TTTTGGCGCA TTTTGCCTTC CTGTTTTTGC	2760
TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG	2820
TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACC	2880
TTTTCCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTATTGA	2940
CGCCGGGCAA GAGCAACTCG GTCGCCGCAT ACATAATTCT CAGAACTACT TGTTGAGTA	3000
CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC	3060

TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC	3120
GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAAC TCGCC TTGATCGTTG	3180
GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC	3240
AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA	3300
ACAATTAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT	3360
TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT CTCGGGGTAT	3420
CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCTGATC GTAGTTATCT ACACGACGGG	3480
GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CTTCACTGAT	3540
TAAGCATTGG TAACTGTCAG ACCAAGTTA CTCATATATA CTTTAGATTG ATTTAAAACT	3600
TCATTTTTTAA TTAAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT	3660
CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC	3720
TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT	3780
ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA AGGTAAGTGG	3840
CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA	3900
CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC	3960
TGCTGCCAGT GCGGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA	4020
TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC	4080
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCCGA	4140
AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG	4200
GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG	4260
ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG	4320
CAACGCGGCG TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC	4380
TGCCTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTTGAGTGAG CTGATACCGC	4440
TCCCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC	4500
AATACGCAAA CCGCCTCTCC CGCGCGGTTG GCCGATTCAT TAATGCAGCT GGCACGACAG	4560
GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT AGCTCACTCA	4620
TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG	4680
CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACG	4724

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGGA GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGACCATGGT GTGTCTGAGG CTCC

24

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGGATCCT CAGCTCAGGA ATCCTCTTG

29

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGGATCCT CACAAGGGCC CTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGGC

27

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCG

26

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA TAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCCTG CGCATGCCCG ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCATAC TGGGCAACCG CCCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTTT CTGTCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCCGAAATCT GCCAAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCGTCC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGAGC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAAGT GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTTT GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGGCCTG GGAGTGACCA GGCAGGAACT	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTCGATGCA CACTCACATT CTTCTCTTAA TACGATAATA AAACCTTCCA	1200
TGAAAAATAT GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCTCCGC	1320
CAATCAGTCG TAAAACAGAA GTCGTGAAA GCGGATAGAA AGAATGTTTG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAAAGTAGTC CAGCCAGTCG CTGTCGAAAC TAATTAAAGTA AATGAGTTTT TCATGTTAGT	1560
TTGCGCTGA GCAACAATTA AGTTTATGTT TCAGTTCGGC TTAGATTTTG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAACTC ATTCTAATAG CTTGGTGTTT	1680
ATCTTTTTTT TTAATGATAA GCATTTTGTC GTTTATACTT TTTATATTTT GATATTAAAC	1740
CACCTATGAA GTTCATTTTA ATCGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATTC	1800
TTTATCAGGA AATTCAGGGA GACGGGGAAG TTAGTATCTA CTAAAAGCCA AACAAATTTCT	1860
TACAGTTTTA CTCTCTCTAC TCTAGAGCTT GGCAGTGGCC GTCGTTTTAC AACGTCGTGA	1920
CTGGGAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG	2100

CATATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCGGACA	2160
CCCGCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG	2220
ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA	2280
ACGCGCGAGA CGAAAGGGCC TCGTGATACG CCTATTTTTA TAGGTTAATG TCATGATAAT	2340
AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTG	2400
TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT	2460
GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCGTG TCGCCCTTAT	2520
TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT	2580

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGCGCGACC TT

32

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTCGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTCGACC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGGATCCC TATGGCCGGA AGGCCTG

27

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCT GTCAGAATGG CCACCAT

27

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTGATATA CAGCACAATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs .
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATTC ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTGGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GCGTACACT TTCCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTC ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCAC T ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCGG GGTAAAAAC ATGTATCACT TTTGTCGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTCTG GTACCATGCC GGAGGAGGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGATCCT CAGGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly  
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: prot in

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe	Val	Arg	Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met
1				5					10			